ELabELN | Template Use Case White Paper

Single-Cell RNA-Seq Experiment Template

Structured Documentation for 10x Chromium Single-Cell Profiling — From Tissue Dissociation Through Capture QC and Seurat Cluster Annotation

APPLIES TO

- Academic and life sciences research laboratories
- Biotechnology and pharmaceutical R&D groups
- Single-cell and genomics core facilities
- Multi-institution consortia and contract research organizations (CROs)

RELEVANT COMPLIANCE & INTEGRITY FRAMEWORKS

- FDA 21 CFR Part 11 — Electronic records and signatures
- EU Annex 11 — Computerized systems in regulated environments
- GAMP 5 — Software validation for regulated industries
- NIH / NSF reproducibility and FAIR data-management requirements

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1. Executive Summary

A single-cell RNA-Seq run turns a piece of tissue into a map of thousands of individual cells, each assigned to a cell type. But the trustworthiness of that map is decided long before the clustering step. It depends on how well the tissue was dissociated into a clean single-cell suspension, on capture-quality metrics — the doublet rate, the mitochondrial fraction, the reads and genes recovered per cell — that determine whether a run is even usable, and on the analysis choices behind every cluster label. A high doublet rate or an unrecorded dissociation protocol can quietly distort which cell types appear and in what proportion, and a cluster called “CD8 T” is only as defensible as the markers and tool version behind the call. When those QC metrics and annotation decisions live in scattered notebooks and an analyst's scripts, the run cannot be reproduced and its cell-type composition cannot be trusted or compared to the next sample.

The ELabELN Single-Cell RNA-Seq Experiment Template solves this by providing a pre-built, fully structured run record that loads from the template library in a single click. It ships with a 10-step 10x Genomics Chromium protocol, validated dissociation references, pre-wired library-QC fields, and typed inputs for tissue source, dissociation method, target cell number, capture rate, library QC, sequencing depth, and per-cluster annotation. The Chromium chip, GEM-X reagents, library-prep kit, and sequencing flow cell link to the ELabELN inventory, and the tamper-evident audit trail captures every dissociation, every chip run, and every QC decision.

This white paper describes what the template contains, the single-cell use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the team, and how a laboratory can deploy it and begin running captures within days.

> **KEY BENEFIT**
> Labs that adopt the scRNA-Seq template stop rebuilding the QC matrix every experiment, capture chip-lot, capture-QC, and cluster-annotation provenance automatically across the wet-lab and computational stages, and gain a queryable, cross-run record — one place that ties every cell-type composition back to its dissociation, its QC metrics, and the analysis that produced it.

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2. What Is Single-Cell RNA-Seq, and Why Does Documentation Matter?

2.1 The Technique

Single-cell RNA sequencing measures gene expression one cell at a time. A tissue is dissociated into a suspension of individual cells, which are partitioned — in the 10x Genomics Chromium system, into nanoliter oil droplets (GEMs), each ideally containing one cell and one barcoded bead. Every cell's transcripts are tagged with a shared cell barcode and unique molecular identifiers (UMIs), pooled into a single library, and sequenced. Computationally, reads are aligned and counted per cell (cellranger), low-quality cells and doublets are filtered on QC metrics, and the remaining cells are clustered and each cluster is annotated with a cell type (Seurat). The result is not an average expression profile but a resolved catalog of the cell types present and their proportions.

This is the method of choice for immune profiling, tumor-microenvironment dissection, developmental atlasing, and perturbation screens. Its power is per-cell resolution; its fragility is that the answer depends on a chain that begins at the bench and ends in code. Dissociation quality governs which cells survive to be captured; the capture QC metrics — captured-cell count, doublet rate, mitochondrial fraction, reads and genes per cell, sequencing saturation — govern whether the data are usable; and the clustering and annotation choices govern what the cell types are called. A poor dissociation or an unrecorded filter threshold can change the biology the run appears to show.

Because a single-cell result is the product of a fragile capture and a chain of analysis decisions, **the dissociation method, the capture-QC metrics, and the per-cluster annotations — with the tools and versions behind them — are what make a run reproducible and comparable to the next sample, which is exactly why they must live in one structured record rather than scattered across the bench and the terminal.**

2.2 The Documentation Problem

Recording single-cell runs across notebooks, an instrument, and analysts' scripts creates a set of interconnected risks:

- The dissociation method and viability — the make-or-break upstream step — are noted informally, so a run distorted by poor dissociation cannot be diagnosed later.
- Capture-QC metrics (captured cells, doublet rate, mitochondrial fraction, reads and genes per cell, saturation) live in a cellranger web summary that is never assembled into a comparable record.
- Chip lot and reagent expiry are not captured against the run, so a batch effect cannot be traced to a chip or reagent lot.
- The QC filter thresholds and the clustering and annotation choices live with the analyst, so a cluster's cell-type call cannot be reproduced or audited.
- Because the workflow spans wet-lab and computational scientists, there is no single timestamped, attributed record of who dissociated, who captured, and who annotated.

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- Prior runs cannot be retrieved to compare QC or cell-type composition across samples, so a drift in capture quality is invisible.

These are the gaps that make single-cell studies hard to reproduce and compare, and they are the gaps this template was designed to close.

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3. Template Overview: What Ships with the Template

The ELabELN Single-Cell RNA-Seq Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for profiling immune-cell heterogeneity in human peripheral blood mononuclear cells (PBMCs) from a single healthy donor using the 10x Genomics Chromium Next GEM Single Cell 3′ v3.1 chemistry, with a 10-step protocol covering PBMC isolation through Seurat-based cluster annotation. The default configuration assumes target capture of 10,000 cells, NovaSeq SP flow-cell sequencing at 28k reads per cell, cellranger count for alignment and UMI quantification, and Seurat v5 for QC, clustering, and cell-type annotation. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of rebuilding the QC matrix from scratch every experiment.

Section	What it pre-populates
Main Text	Study design, dissociation notes, and expected cell-type composition, authored in the TinyMCE rich-text editor and linked to the upstream isolation.
Extra Fields	Twelve structured, typed fields grouped as Sample, Capture & Library, and Sequencing & QC — tissue, donor, dissociation method, target cells, captured cells, doublet rate, mean reads per cell, median genes per cell, mitochondrial fraction, saturation, and number of clusters. Typed values make library QC and biology outcomes queryable across runs.
Steps	A 10-step workflow checklist covering PBMC isolation through Seurat clustering. Each tick is timestamped to the audit trail, and the Chromium run is auto-logged.
Compounds	The Chromium chip, GEM-X reagents, library-prep kit, NovaSeq flow cell, and dissociation enzymes pre-linked from the compound database, with the chip lot carried in automatically and reagent expiry shown inline.
Links & Resources	Pre-wired to the lab's scRNA-Seq SOP v1.8, the 10x Chromium 3′ v3.1 user guide, and the Seurat pipeline reference docs.
Storage & Files	LN_2 PBMC cryovial archive and library aliquot storage, plus labelled attachment slots for BCL + FASTQ paths and Seurat object files (H5 + RDS).

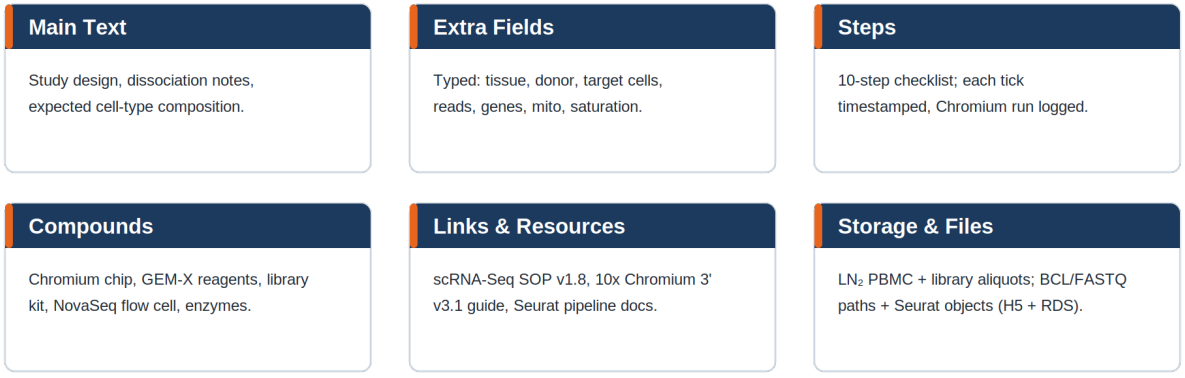
Main Text
Study design, dissociation notes, expected cell-type composition.
Extra Fields
Typed: tissue, donor, target cells, reads, genes, mito, saturation.
Steps
10-step checklist; each tick timestamped, Chromium run logged.
Compounds
Chromium chip, GEM-X reagents, library kit, NovaSeq flow cell, enzymes.
Links & Resources
scRNA-Seq SOP v1.8, 10x Chromium 3' v3.1 guide, Seurat pipeline docs.
Storage & Files
LN₂ PBMC + library aliquots; BCL/FASTQ paths + Seurat objects (H5 + RDS).

Figure 1. The six ELabELN experiment sections pre-populated by the single-cell RNA-Seq template.

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3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete wet-lab, instrument, or computational action and writes a timestamped, user-attributed entry to the audit trail when checked off. The Chromium run is auto-logged, and the alignment and clustering steps are performed in external tools, with their outputs and versions recorded as typed fields.

Step	Action	What it captures
1	Isolate PBMCs	Tissue; donor
2	Dissociate & count	Dissociation method; viability
3	Load Chromium (GEM capture)	Target cells; chemistry; chip lot
4	Reverse transcription (in-GEM)	Barcoding / RT
5	cDNA amplification	Amplification
6	Library prep	Library QC
7	Sequence (NovaSeq)	Sequencing depth; flow cell (run auto-logged)
8	cellranger count	Alignment + UMI; captured cells (external)
9	QC & filter (Seurat)	Doublet rate, mitochondrial %, genes/cell
10	Cluster & annotate (Seurat)	Clusters; cell-type annotation (external); e-signature

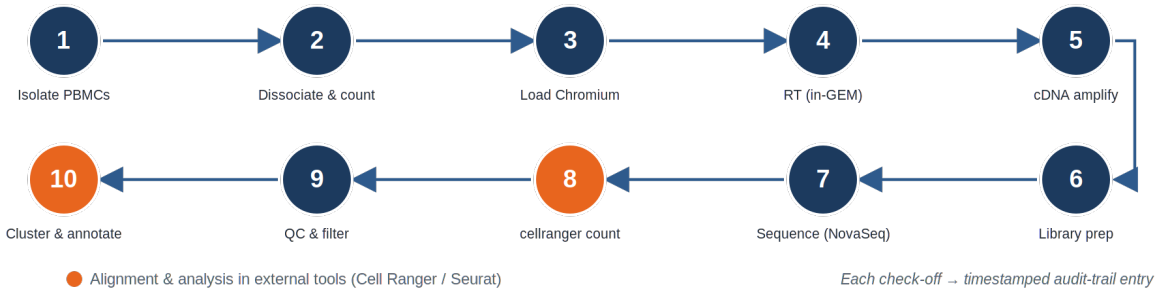

Figure 2. The 10-step 10x Chromium single-cell workflow — orange steps are the alignment and analysis performed in external tools (Cell Ranger / Seurat); every check-off writes a timestamped entry to the ELabELN audit trail.

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4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic, biotechnology, and pharmaceutical labs running single-cell profiling. It is configured around a recognizable reference — an immune-profiling run on human PBMCs — but the scenarios it serves span the single-cell bench and its downstream analysis.

4.1 Immune Profiling (Primary Use Case)

The core scenario: resolving the immune cell types present in a sample and their proportions. The template captures the dissociation, the capture QC, and the per-cluster annotations in one structured record, so a cell-type composition is fully reconstructable — which dissociation, which QC thresholds, which annotation method — rather than a cluster plot detached from the run that produced it.

4.2 Tumor-Microenvironment Dissection

Dissociated tumors yield a mix of malignant, immune, and stromal cells whose proportions carry the biology. The template's tissue and dissociation fields, and its per-cluster annotation, capture the heterogeneity in a form that is comparable across tumors and conditions.

4.3 Developmental Atlasing

Atlas projects profile many samples across tissues or time to build a reference of cell states. Because capture QC and annotations are structured and queryable, samples can be assembled into an atlas with consistent, documented QC and cell-type calls.

4.4 Perturb-seq and Screens

Perturbation screens read out the transcriptional consequences of many genetic or chemical perturbations at single-cell resolution. The template's structured capture and analysis fields document the design and QC so perturbation effects are interpreted against a known baseline.

4.5 Cross-Condition Differential Abundance and Cross-Run QC

Comparing cell-type proportions across conditions — or simply tracking capture quality across many runs — depends on comparable, queryable records. A lab can pull every run on a chemistry version or chip lot and compare doublet rate, genes per cell, and cell-type composition side by side, catching a dissociation or capture problem before it confounds a conclusion.

4.6 Consortia, Multi-Team, and CRO Settings

Single-cell work is collaborative and often spans institutions. Because every ELabELN edition includes unlimited users, the PI, computational biologists, wet-lab scientists, rotating researchers, and consortium collaborators can all work from the same record. Granular permissions let project leads control who can edit run records versus only review them — the role separation a consortium or CRO needs so the wet-lab and computational contributors each own their stage.

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5. Dependencies and Connected Workflows

The scRNA-Seq template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, external, and downstream — that give the run record its full scientific and provenance value.

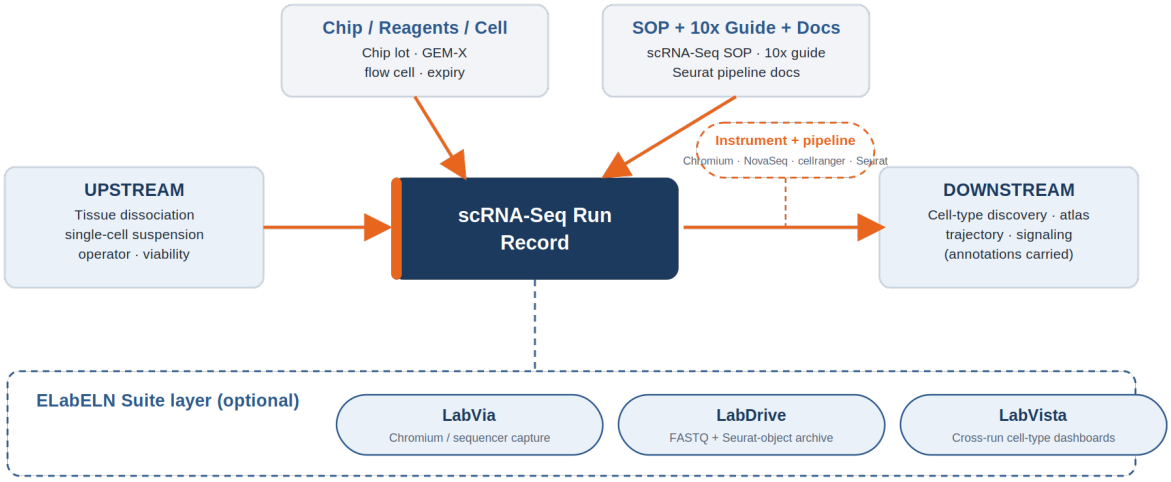

Figure 3. The template connects an upstream tissue dissociation, parallel inventory and SOP/guide/pipeline systems, the external instrument-and-pipeline stack, and downstream discovery and atlasing workflows.

5.1 Upstream: Tissue Dissociation and Isolation

Every run begins with a single-cell suspension — PBMCs, dissociated tumor, or another tissue. The template links to the upstream isolation and dissociation record, so opening a run surfaces the tissue source, the dissociation method, and the viability, operator, and date, anchoring every captured cell to the material and the dissociation behind it. Because dissociation quality is the single most consequential upstream variable in single-cell work, this link matters more here than in almost any other assay.

5.2 Parallel: Chip, Reagent, and Flow-Cell Inventory

The Compounds section links the Chromium chip, GEM-X reagents, library-prep kit, NovaSeq flow cell, and dissociation enzymes directly to the ELabELN inventory. Because chip and reagent lots drive capture behavior, this traceability is decisive. Through the link the record automatically carries:

- **The chip lot, carried automatically**, with chip-history references, so a capture problem can be traced to a specific chip or lot.
- **Reagent expiry, shown inline**, so a run is not started against an expired GEM-X or library-prep reagent.
- **Stock levels**, with low-stock warnings before a run, so a capture is not begun without the reagents to finish it.

Barcode and QR scanning can populate these links from the physical chip and kit, keeping lot capture effortless.

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5.3 Parallel: SOPs, the 10x Guide, and Pipeline Docs

The Links section connects the run to the lab's version-controlled scRNA-Seq SOP (v1.8 by default), the 10x Chromium 3′ v3.1 user guide, and the Seurat pipeline reference docs. Because these are version-controlled in ELabELN, every run records exactly which protocol, chemistry guide, and analysis pipeline it followed — the anchors that reproducibility and cross-run comparison depend on.

5.4 External: The Instrument and Analysis Pipeline

The Chromium instrument performs the capture, the NovaSeq sequences the library, cellranger aligns reads and quantifies UMIs, and Seurat performs QC, clustering, and annotation. ELabELN is the system of record around that pipeline: the tissue, dissociation, target and captured cells, doublet rate, reads and genes per cell, mitochondrial fraction, saturation, and cluster count are captured as typed fields; the per-cluster cell counts and assigned cell types (CD4 T, CD8 T, NK, B, Monocyte, mDC, pDC, Platelet) live in the spreadsheet editor; and the BCL and FASTQ paths and the Seurat object files (H5 + RDS) attach to the record. The dissociation, the raw data, and the annotated result stay together in one place.

5.5 Downstream: Discovery, Atlasing, and Cross-Run

The annotated clusters feed cell-type discovery, trajectory and cell-cell-signaling analysis, atlasing, and reporting, and — because the QC metrics and annotations are typed and queryable — cross-run and cross-condition analysis across a shared resource. A drift in capture quality or a batch effect shows up when runs are compared, not after a conclusion is drawn.

5.6 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures run data directly from the Chromium instrument and sequencer; LabDrive adds metadata search, versioning, and role-based access across FASTQ and Seurat-object archives; and LabVista builds cross-run cell-type-composition dashboards on the structured QC and annotation metadata. The same audit trail and data-integrity controls span all layers.

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6. How the Team Benefits

The template is built to deliver value across both the wet-lab and computational stages, not just at the bench. The benefits compound with every run a lab performs.

6.1 Start From a Tested Baseline, Not a Blank QC Matrix

The scaffold — protocol, typed QC fields, reagent links, SOP, 10x guide, and pipeline docs — is already built. The team edits a working configuration to match the tissue and design they actually run, rather than rebuilding the QC matrix from scratch every experiment. The first run is faster, and every subsequent one is consistent with it.

6.2 Document by Doing, Across Both Stages

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the work, and the Chromium run is auto-logged. Dissociation, capture, and analysis are documented as they occur, by whoever performs them — with no separate write-up to reconstruct later.

6.3 Never Lose Dissociation, QC, or Annotation Provenance Again

Because the dissociation is a structured field, the reagents are linked to inventory, and the QC metrics and cluster annotations are typed, the make-or-break upstream step, the chip lot, and every QC and annotation decision are captured permanently on every run. When a cell-type composition is questioned, the provenance is on the record — closing the most consequential single-cell gap by default.

6.4 Cross-Run Comparisons You Can Query

Typed capture-QC and annotation fields make the study queryable. A team can pull every run on a chemistry version or chip lot, compare doublet rate, genes per cell, and cell-type composition, and catch a dissociation or capture problem early — instead of discovering it after the study is assembled.

6.5 Audit-Ready Records with Role Separation

The tamper-evident audit trail, version-controlled linkage, electronic signatures, and granular permissions mean the record that results from normal use is already structured to support reproducibility documentation, multi-PI consortium collaboration, and FDA 21 CFR Part 11 review when the lab's quality system requires it — with the wet-lab and computational contributors each owning their stage of the record.

> **AT THE BENCH, IN PRACTICE**
> A wet-lab scientist opens the template, records the tissue and dissociation method, scans the Chromium chip to capture its lot, and checks off isolation, dissociation, and capture as the viability and target-cell count go into typed fields. The Chromium and NovaSeq runs auto-log. The computational biologist then records the captured-cell count, doublet rate, mitochondrial fraction, and genes per cell from cellranger, filters and clusters in Seurat, and enters the per-

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> cluster cell-type annotations with the Seurat object attached. Months later, comparing runs, the PI queries every run on that chemistry and sees whether the QC and cell-type proportions held.

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7. Capture QC and Cluster Annotation

7.1 The Default Reference: A PBMC Immune-Profiling Run

The template ships configured for immune profiling of human PBMCs from a single healthy donor: 10x Chromium Next GEM Single Cell 3′ v3.1 capture targeting 10,000 cells, NovaSeq SP sequencing at 28k reads per cell, cellranger for alignment and UMI counting, and Seurat for QC, clustering, and annotation. After filtering on the capture-QC metrics, the cells cluster into the expected PBMC populations — CD4 T, CD8 T, NK, B, monocytes, dendritic-cell subsets, and platelets — each annotated on the UMAP. This concrete reference demonstrates the full capture-to-annotation workflow out of the box; swap the tissue, chemistry, or analysis tool to match what your lab runs.

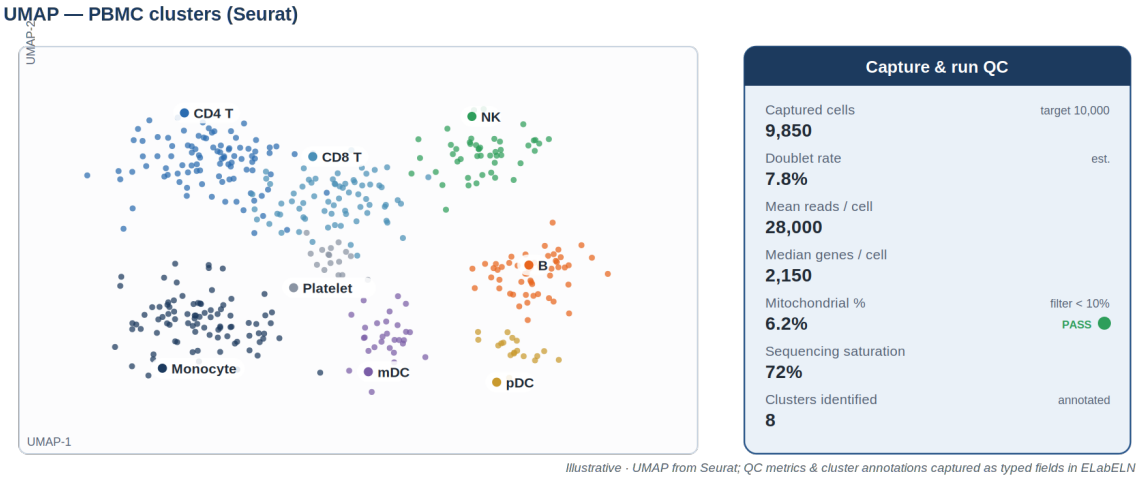

Figure 4. An annotated UMAP of the PBMC clusters alongside the capture and run-QC metrics that gate a usable run. Illustrative; the UMAP comes from Seurat, and the QC metrics and cluster annotations are captured as typed fields in ELabELN.

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7.2 How the Template Handles QC, Clusters, and Annotation

The tissue, donor, dissociation method, target and captured cells, doublet rate, mean reads and median genes per cell, mitochondrial fraction, saturation, and cluster count are all captured as typed fields, and the per-cluster cell counts and assigned cell-type labels live in the spreadsheet editor for cross-sample comparison. The alignment and analysis run in cellranger and Seurat, with the BCL and FASTQ paths and Seurat object files attached to the record. Annotation can come from manual curation, marker-gene scoring (Seurat's FindAllMarkers), or automated tools (SingleR, scType, Azimuth) — and whichever method is used, the resulting labels and the cluster count are recorded as typed fields. Because the QC metrics and annotations are structured and queryable, cross-run comparison is straightforward: query every run on a chemistry version or chip lot and review capture quality and cell-type composition side by side.

Element	Default configuration	Editable to
Tissue	PBMC (single healthy donor)	Dissociated tumor, brain, lung, intestine, organoid
Chemistry	10x Chromium 3′ v3.1	5′ v2, multiome, fixed RNA
Target cells	10,000	1,000 – 30,000
Analysis	cellranger + Seurat	Scanpy, Scran
Design	Single-sample	Multiplexed (CellPlex, HTO); multi-modal (CITE-Seq, ATAC)

Figure 5. The template's default configuration — fully editable for any tissue, chemistry, capture target, analysis tool, or study design.

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8. Configuring the Template for Your Run

Adapting the template to a different tissue or design is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Swap the Tissue Source

Change the tissue (PBMC, dissociated tumor, brain, lung, intestine, organoid) and its dissociation method by editing the sample and capture sections. The per-cluster annotation extends to tissue-specific cell types beyond the default PBMC set.

8.2 Change the Chemistry

Switch the chemistry — 3′ v3.1, 5′ v2, multiome, or fixed RNA — by editing the capture section. If the chips and reagents already exist in the ELabELN compound database, simply re-link them; their lots flow in automatically.

8.3 Change the Scale, Depth, Analysis, and Modality

Adjust the target cell number from 1,000 to 30,000 and the sequencing depth to match your design, change the analysis tool (Seurat, Scanpy, Scran), and move from single-sample to multiplexed (CellPlex, HTO) or multi-modal (CITE-Seq, ATAC) runs by editing the capture section.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent run opens from your configured, version-controlled design, and separate versions can be maintained for different tissues, chemistries, or modalities.

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9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the single-cell RNA-Seq template.** From the template library, select the scRNA-Seq template and click “Use This Template.” An editable instance opens immediately.
4. **Add your chips, reagents, and flow cells to the inventory.** Enter your Chromium chips, GEM-X reagents, library-prep kits, flow cells, and dissociation enzymes with lot numbers and LN_2 / storage locations. This is a one-time setup step.
5. **Link your SOP, 10x guide, and pipeline docs.** Upload your scRNA-Seq SOP, and connect the 10x Chromium user guide and Seurat pipeline docs to the template's Links section.
6. **Customize the template for your run.** Edit the tissue, chemistry, target cell number, sequencing depth, and analysis tool, then save as a private team version.
7. **Run your first capture.** Open your saved template, complete the 10-step checklist across dissociation, capture, and analysis, attach the FASTQ paths and Seurat object, and have the PI sign off electronically.

TYPICAL TIMELINE

Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; chip/reagent/flow-cell inventory populated; SOP, 10x guide, and pipeline docs linked. Day 3–4: Template configured and saved as a private version for your tissue and design. Day 4–5: First run documented in ELabELN with dissociation, capture QC, and cluster annotations captured and an e-signature.

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9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
Single-cell RNA-Seq template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Chip / reagent / flow-cell inventory with lot tracking	Included	Included
SOP, 10x guide & Seurat pipeline linking	Included	Included
BCL/FASTQ paths + Seurat object attachments	Included	Included
LabVia direct Chromium / sequencer capture	—	Suite layer
LabDrive FASTQ + Seurat-object archive search & versioning	—	Suite layer
LabVista cross-run cell-type-composition dashboards	—	Suite layer

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10. Frequently Asked Questions

Can I configure the template for my tissue and design?

Yes. Every section is editable. Swap in different tissues (PBMC, dissociated tumor, brain, lung, intestine, organoid), change the chemistry (3′ v3.1, 5′ v2, multiome, fixed RNA, CellPlex multiplexed, CITE-Seq), adjust the target cell number from 1,000 to 30,000, change the sequencing depth, or move from single-sample to multiplexed or multi-modal runs. Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

How does the template differ from the bulk RNA-Seq template?

The bulk RNA-Seq template profiles average gene expression across a pooled sample, supporting differential expression between conditions. This single-cell template resolves expression per cell, allowing cell-type discovery, heterogeneity dissection, trajectory analysis, and cell-cell signaling. Both share the sequencing-readout pattern, but the upstream capture (10x emulsion vs bulk RNA prep) and the downstream analysis (Seurat clustering vs DESeq2) are different.

Does the template support cluster annotation?

Yes. The spreadsheet editor captures the per-cluster cell count and assigned cell-type label (CD4 T, CD8 T, NK, B, monocyte, dendritic-cell subsets, platelet, plus tissue-specific types). The typed Sequencing & QC fields hold the cluster count and overall QC roll-up. Annotation can come from manual curation, marker-gene scoring (Seurat's FindAllMarkers), or automated tools (SingleR, scType, Azimuth).

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, computational biologists, wet-lab scientists, rotating researchers, and consortium collaborators can all use the template without per-seat charges. Granular permissions let project leads control who can edit run records versus only review them.

How quickly can my lab start running scRNA-Seq in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the tissue, chemistry, capture target, and analysis pipeline editable to match the experiments your lab actually runs.

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11. Conclusion

The ELabELN Single-Cell RNA-Seq Experiment Template is not simply a digital version of a cellranger web summary. It is a structured, audit-ready, searchable record that connects to your chip and reagent inventory, your SOPs, 10x guide, and pipeline docs, the tissue the run profiled, your Chromium instrument and analysis pipeline, and the discovery and atlasing the results feed — and, in the Suite edition, cross-run cell-type-composition dashboards. It turns a fragile, multi-stage capture into a single record whose dissociation, QC metrics, and cluster annotations are captured, comparable, and defensible.

For a laboratory that runs single-cell regularly, the benefit compounds with every capture. Dissociation methods, capture-QC metrics, and cell-type annotations accumulate into one queryable, cross-run history. Every chip lot and reagent is traceable. Every chemistry and tool version is documented. Every stage is timestamped and attributed to whoever performed it — so a poor dissociation or an unrecorded QC threshold can no longer quietly distort the biology, and a drift in capture quality is caught before it confounds a conclusion.

The template is available to all ELabELN subscribers today. A new instance is live in one to two business days, and the first structured run is typically documented within a week of account creation.

> **GET STARTED**
> Visit elabeln.com/get-started to request your ELabELN instance, or contact LabLynx at 866.522.5969 or info@lablynx.com. Load the single-cell RNA-Seq template, configure it for your tissue and design, and run your next capture from a tested, audit-ready baseline.

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